<u>SUBSTITUTE</u>

<u>SPECIFICATION AND CLAIMS INCLUDING AMENDMENTS</u>

<u>MADE UNDER PCT ARTICLE(S) 19/34</u>

<u>(also includes Abstract, Sequence Listing, Drawings</u>

<u>and Declaration)</u>

Title of Invention:

ALTERED INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS

Attorney Docket No. A20-073

1

ALTERED INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS

FIELD OF THE INVENTION

This invention relates to an altered Insulin-like Growth Factor Binding Protein (IGFBP)

5   with reduced IGF (Insulin-like Growth Factor) release characteristics. The IGFBP of the

invention is proposed to be useful for therapeutic purposes, such as treatment of certain

cancers. A specific form of the invention relates to an altered IGFBP-2.

BACKGROUND TO THE INVENTION

10 Insulin-like growth factors (IGF-I and IGF-II) are small, highly-related proteins (~7.5

kilodaltons) which mediate anabolic, mitogenic and anti-apoptotic activities in a wide

variety of cell types. These actions result from IGF interaction with and subsequent

activation of the type 1 IGF receptor (IGF1R) (Sepp-Lorenzino, (1998), Baserga, 1999).

A second unrelated receptor (the type 2 IGF receptor or IGF2R) has the major function of

15 regulation of IGF-II levels by internalisation and degradation (Wang et al., 1994) and

current evidence suggests that the IGF2R acts as a tumour suppressor of IGF-II-

dependent tumours (Braulke, 1999).

IGFs are produced by the liver, providing circulating IGF, and are also secreted locally in

20 most tissues. A family of 6 high-affinity IGF binding proteins (IGFBP-1 to -6) act to

increase the half-life of IGFs in circulation (predominantly as the IGFBP-3·ALS·IGF

complex) and also to transport IGFs to target tissues. Within target tissues IGFBPs can

either enhance or inhibit IGF action. IGFBPs can inhibit the interaction of IGF by

blocking binding to the IGF1R. However, under certain circumstances IGFBPs can

25 release IGF, thereby making IGF available for binding to the IGF1R. This results in an

enhancing effect on IGF action. Release mechanisms include 1) proteolysis of the

IGFBPs and 2) IGFBP binding to the extracellular matrix (ECM), both of which lower

their affinity for IGF. Extracellular matrix binding is also believed to assist the

localisation of IGF close to the cell surface and therefore near IGF1Rs. The outcome of

30 IGFBP action is controlled by a balance between local proteolytic activity and the

binding of IGFBPs to the ECM.

Substantial evidence (*in vivo* and *in vitro*) implicates insulin-like growth factors (IGFs) and IGF binding proteins (IGFBPs) in cancer. Many tumour cells (including prostate and breast) secrete more IGF-II and IGFBP-2 than their normal counterparts and their serum levels commonly rise as cancers progress (Cohen *et al.*, (1994); Thrasher *et al.*,(1996);

5 Ho *et al.*, (1997); Chan *et al.*, 1998). IGF secreted by tumour cells binds to the Type 1 IGF receptor potentiating tumourigenesis and metastasis (DiGiovanni *et al.*, 2000).

The proteolysis of IGFBP-2 has been detected under a number of normal and abnormal physiological conditions. For example, IGFBP-2 fragments have been detected in human

10 milk and cleavage occurred predominantly in the linker region between the N- and C-domains and including sites at residues 168 and 180/181 of hIGFBP-2 (Ho and Baxter, 1997; Elminger *et al.*, 1999). Proteolysed IGFBP-2 is also found in serum during pregnancy. IGFBP-2 is also cleaved by proteases produced by cancer cells (Michell *et al.*, 1997). The specific cancer cell proteases have not been well characterised although

15 Cathepsin D produced *in vitro* by prostate epithelial cells has been shown to degrade IGFBP-2 (Kanety *et al.*, 1993; Nunn *et al.*, 1997). Preferential proteolysis of IGFBP-2 has been demonstrated in colonic cancers (Michell *et al.*, 1997) and neuroblastoma cells (Menouny *et al.*, 1997). Specific cleavage sites have not been described for proteolytic products generated by cancer proteases.

20

Protease cleavage sites have been identified in the IGFBP-3, -4 and –5 sequences. Proteolysis is generally within the linker regions of these proteins although it can be in the C-domain. Protease resistant IGFBP-4 and IGFBP-5 (Imai *et al.*, 1997) have been generated by mutating specific residues at cleavage sites or by deletion of some linker

25 region residues (deletion of 121-141 of IGFBP-4 rendered it resistant to a protease in pregnancy serum (Byun *et al.*, 2000).

IGFBP-2 binds to human fibroblast extracellular membrane preparations (Arai *et al.*, 1996) and glycosaminoglycans (Russo *et al* 1997, Arai *et al.*, 1996). There are 2 potential

30 matrix binding sites within the IGFBP-2 sequence. Current evidence suggests that the basic region of hIGFBP-2 (residues 227-244), corresponding to residues 201-218 of hIGFBP-5, may act as a site for matrix binding (Arai *et al.*, 1996). Using a synthetic

peptide based on residues 201-218 of hIGFBP-5 (residues known to be important for matrix binding) Arai *et al.*, 1996, inhibited IGFBP-2 binding to heparin-Sepharose. Hodgkinson *et al.*, (1994) predicted a glycosaminoglycan (GAG) binding site in IGFBP-2 based on a short GAG-binding consensus sequence described by Cardin and Weintraub

5   (1989). This XBBXBX (B=basic, X=undefined) motif at residues 179-184 of hIGFBP-2 lies in the central domain. There is no published evidence that this motif plays a role in GAG binding.

For the purposes of this specification the word "comprising" means "including but not

10   limited to", and the word "comprises" has a corresponding meaning. Also a reference within this specification to a document is not to be taken as an admission that the disclosure therein constitutes common general knowledge in Australia.

SUMMARY OF THE INVENTION

15   This invention arises from the alteration of IGFBP-2 in a manner that inhibits the release of IGF-I and IGF-II. The inhibition of release results from the introduction of changes to the IGFBP-2 resulting in reduced binding to extracellular matrix (ECM) and reduced susceptibility to proteolysis by one or more proteases. This altered IGFBP-2 is proposed to be useful for its ability to inhibit growth of IGF-dependent tumours such as colon,

20   prostate and breast cancers. This is to the inventor's knowledge the first time that an altered IGFBP has been constructed to contain both reduced ECM binding and reduced proteolytic susceptibility and the first time that this combination has been shown to be effective at inhibiting the release of IGF-I and IGF-II. It is proposed that this approach will be effective not only for IGFBP-2 but also for other IGFBPs. Additionally this is to

25   the inventor's knowledge the first time that there have been functional data to show the location of the two ECM binding sites for IGFBP-2, and a demonstration that these together with alteration of proteolysis sites result in inhibition of the release of IGF-I and IGF-II. Additionally this is the first time to the inventor's knowledge that an overlapping IGF and ECM binding site has been altered in a manner that still allows IGF binding but

30   not ECM binding.

The invention might in a first broad aspect be said therefore to reside in an altered IGFBP-2 molecule able to effect binding of IGF-I or IGF-II with high affinity characterised in an inhibited release of IGF on contact with extracellular matrix or exposure to a protease.

5

In a second form of the first aspect of the invention might be said to reside in an altered IGFBP molecule able to effect binding of IGF-I or IGF-II with high affinity characterised in an inhibited release of IGF on contact with extracellular matrix and exposure to a protease.

10

Cleaved IGFBP-2 has greater than 10 fold weaker affinity for IGF (Carrick, 2001). It is desirable for the altered IGFBP-2 to have at least to have an affinity for IGF-I equivalent to the IGF type 1 receptor which is 10 fold lower than that of native IGFBP-2 for IGF-I. This allows effective competition with the receptor for IGF binding and the term high

15 affinity binding of IGF should be understood in that context.

Regions required for IGF binding have not been fully elucidated however considerable effort has been made to define these regions. Thus for example we (Hobba et al., 1998) and others (Zeslawski et al., 2001) have identified residues in the distal part of the N-

20 domain involved in IGF binding. Similarly, the minimum C-domain length of IGFBP-2 required for IGF binding has been described (Forbes et al., 1998). WO 00/23469 also describes the IGF binding domain which document is incorporated herein in its entirety by reference. Methods for assaying IGF binding are known in the art and can be readily employed to ascertain whether the altered IGFBP is able to bind IGF or not.

25

The inventor has identified two ECM sites for IGFBP-2 and shown that mutations in these lead to reduced heparin binding. The first ECM site for IGFBP-2 spans sequence 179-184 and consists of the sequence PKKLRP [SEQ ID No 1] and was originally proposed on the basis of homology with the consensus sequence for matrix binding

30 proteins (namely XBBXBX, Hodgkinson et al., 1994). The second ECM binding sequence of IGFBP-2 identified is at 227-244 by homology with IGFBP-3 and IGFBP-5 and consists of sequence KHGLYNLKQCKMSLNGQR [SEQ ID No 2]. Suitable

reference sequence is available from sequence databases. Thus the nucleotide sequence of cDNA of human IGFBP-2 might be accessed from the NCBI sequence database as accession number NM000597. Suitable amino acid sequence predictions can be made from the nucleotide sequence.

5

The invention might also in a third form of the first aspect be said to reside in an altered IGFBP-2 molecule able to effect binding of IGF-I or IGF-II with high affinity said IGFBP-2 molecule having alterations in any one or more amino acids in both ECM binding sites, a first ECM binding site being located at sequence 179 to 185 and a second

10   ECM binding site being located at sequences 227 through 244, the alterations separately and together inhibiting the binding of the IGFBP-2 to ECM.

Preferably residues between 227 and 236 are substitution mutations because it is thought that at least part of this site may also be important for IGF binding. Whereas the 179-185

15   alteration may be achieved by deletion, inversion, substitution or other gross alteration, however preferably this is altered by amino acid substitution.

Generally substitution of a basic amino acid for an amino acid of different character, that is either neutral, or acidic is found generally to have a disrupting effect on matrix binding

20   motifs.

It is found by the inventor that utilising the mutations so far introduced into IGFBP-2 that alteration of one of the two ECM sites alone is not sufficient to totally abolish ECM binding. Whilst the present invention preferably provides for the alteration of both ECM

25   sites, the invention might also encompass the provision of alteration in one only of the ECM binding sites, and perhaps in combination with an altered protease cleavage and/or binding site.

Set out below are sequences shown or proposed to be the ECM binding sites for all six

30   IGFBPs.

ECM binding sites (in the C-domain between the 14th and 16th cysteine residues)

```
IGFBP-3    CDKKGFYKKKQCRPSKGRKRGFC  [SEQ ID No 3]  (Firth, 1998)

IGFBP-5    CDRKGFYKRKQCKPSRGRKRGIC  [SEQ ID No 4]  (Arai, 1996b)

IGFBP-2    CDKHGLYNLKQCKMSLNGQRGEC  [SEQ ID No 5]
              *       *  *       *
```

5
```
IGFBP1     CNKNGFYHSRQCETSMDGEAGLC  [SEQ ID No 6]

IGFBP4     CDRNGNFHPKQCHPALDGQRGKC  [SEQ ID No 7]

IGFBP6     CDHRGFYRKRQCRSSQGQRRGPC  [SEQ ID No 8]
```
*=conserved positively charged residues

10 Sites for IGFBP 3 and IGFBP 5 have been published previously the present data establishes the binding site for IGFBP-2 and the sites for IGFBP1, 4, and 6 are suggested by reason of amino acid alignment.

The invention might also encompass an altered IGFBP-1,- 4, or -6 having an alteration in

15 the ECM binding sites.

Alternatively in this first aspect of the invention it might be that a satisfactory decreased release of IGF is achieved solely by inhibition of ECM binding by amino acid substitution at the second ECM binding site. Such decreased release might be the result

20 of the close association between the IGF binding site and the second ECM binding site, and therefore the first aspect of the invention might reside in an altered IGFBP molecule and perhaps preferably an IGFBP-2 molecule that has one or more amino acid substitutions in the ECM binding site that still allows binding of IGF, whilst still inhibiting binding of ECM and thereby also inhibiting IGF release.

25

It is thought that the positively charged residues are important for binding and thus substitution of these are likely to result in inhibition of binding. The substitution might be a non conservative substitution such as the following alanine (A) substitutions for lysine (K).

30

Site 1		Site 2	
PKKLRP	[SEQ ID No 9]	KHGLYNLKQCKMSLNGQR	[SEQ ID No 14]
PAKLRP	[SEQ ID No 10]	AHGLYNLKQCKMSLNGQR	[SEQ ID No 15]
5 PKALRP	[SEQ ID No 11]	KHGLYNLAQCKMSLNGQR	[SEQ ID No 16]
PKKLAP	[SEQ ID No 12]	KHGLYNLKQCAMSLNGQR	[SEQ ID No 17]
PAALAP	[SEQ ID No 13]	AHGLYNLAQCAMSLNGQR	[SEQ ID No 18]

Substitutions of the lysine residues by other amino acids might also be contemplated.

10

The altered IGFBP-2 of the first aspect of the invention preferrably also has an alteration at any one or more proteolytic cleavage sites whereby to inhibit the release of an IGF when subjected to a protease specific for the proteolytic cleavage site.

15 A preferred form of the first aspect of the invention comprises substitution mutations at the first and second ECM binding sites, perhaps those referred to above, together with any one or more deletions in the linker domain that remove one or more proteolytic cleavage sites.

20 As indicated above in certain aspects the invention encompasses alterations that inhibit IGF release on exposure to one or more proteolytic enzymes. Many proteolytic enzymes to which IGFBPs are susceptible have as their target the linker domain. The proteolytic enzyme that the altered IGFBP is exposed to on delivery for therapeutic purposes may differ depending on the conditions to be treated. It is known that tumour cell lines vary in 25 the proteolytic enzymes they produce. It has been shown by the inventor that a substantial deletion in the linker domain of IGFBP-2 leads to resistance to proteolytic cleavage whilst at the same time maintaining protein stability and maintaining IGF binding at high affinity. A preferred alteration of the IGFBP that leads to protease resistance is therefore one or more deletions within the linker domain. The size of the 30 deletion or deletions may be varied. It has been found by the inventor that a deletion of substantially all of the linker region still led to IGF binding. With a deletion of

substantially all of the linker domain it is preferred that amino acids from about 180 through to 191 are maintained.

Smaller deletions may also be suitable for removal of sites that make the IGFBP
5   susceptible to proteolysis, thus deletions of amino acids about 110 through to about 170 has resulted in a decrease susceptibility to proteolysis.

Resistance to proteolysis may also be achieved by more targetted alteration to sites important for proteolytic cleavage or binding.
10

Substitution of residues other than those involved in proteolysis or ECM binding might also be contemplated, and these might be conservative substitutions or non-conservative substitutions, deletions, duplications, inversions and other rearrangements, provided that the altered IGFBP is still capable of high affinity IGF binding. Additionally the altered
15   IGFBP might have additional changes such as glycosylations or other chemical modifications.

The proteins may be a fusion protein which assists in the purification, thus the protein may include a C terminal 6 histidine tag which provides for nickel affinity purification.
20   Other fusion purification systems are also known and may be used. For bacterial systems a fusion protein may include a signal sequence, such as one derived from ompA, adapted to have the protein secreted through the surface of the cell.

In a second aspect the invention might be said to reside in a nucleic acid encoding one or
25   more of the proteins or amino acid sequences of the first aspect of the invention. In a preferred form the nucleic acid is carried by a vector, the vector having nucleic acid operably linked with a control sequence including a promoter for transcription leading to expression of the protein or amino acid. Any one of the very many known vectors for that purpose may be used. Alternatively the vector may be used simply to introduce the
30   nucleic acid encoding the altered IGFBP into a host cell for integration into a chromosome host cell, and might therefore be a retroviral expression vector.

In a third form the invention might be said to reside in a recombinant cell carrying a vector or the nucleic acid of the second aspect of the invention. The host cell might be intended for expression of the altered IGFBP which can thus be produced and purified such that the purified protein may be then separately used or administered as desired.

5 The host cell might be bacterial, yeast, plant or mammalian. Alternatively the host cell may be intended for introduction into a treated animal such as a human for gene therapy purposes.

In a fourth form the invention might be said to reside in a pharmaceutical composition.

10 The composition including the altered IGFBP-2 of the first aspect of the invention as an active component. The pharmaceutical composition may be formulated in accordance with an approved method, and may include a carrier which may or may not be fused to the altered IGFBP, or conjugated with the altered IGFBP. The composition may additionally include other medicinal agents, pharmaceutical agents, adjuvants, diluent,

15 excipients and the like.

The invention might in a fifth form also be said to reside in a method for decreasing serum and/or tissue levels of biologically active IGF-I or IGF-II by administering to a mammal an amount of altered IGFBP of the first aspect of this invention effective to

20 inhibit the release of IGF-I or IGF-II from the altered IGFBP and thereby decrease serum and tissue levels of biologically active IGF-I or IGF-II.

The fifth aspect of the invention contemplates the expression of exogenous nucleic acid encoding the altered IGFBP-2 in one or more cells of the animal of human patient, as a so

25 called gene therapy approach.

Generally, gene therapy is used to increase (or overexpress) altered IGFBP-2 levels in the mammal. Nucleic acids which encode IGFBP-2 be used for this purpose. Several nucleic acid molecules may be generated using the degeneracy of the genetic code that encodes

30 the desired amino acid sequence.

There are two principal approaches to getting the nucleic acid (optionally contained in a vector) into the patient's cells for purposes of gene therapy: *in vivo* and *ex vivo*. For *in vivo* delivery, the nucleic acid is injected directly into the patient, usually at the site where the viperine is required. Preferably this might be in the liver. For *ex vivo*

5   treatment, the patient's cells are removed, the nucleic acid is introduced into these isolated cells and the modified cells are administered to the patient either directly or, for example, encapsulated within porous membranes which are implanted into the patient. See, e.g. U.S. Pat. Nos. 4,892,538 and 5,283,187.

10   There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate

15   precipitation method, etc. A commonly used vector for *ex vivo* delivery of the gene is a retrovirus.

In vivo nucleic acid transfer techniques include transfection with viral vectors (such as adenovirus, Herpes simplex I virus, or adeno-associated virus) and lipid-based systems

20   (useful lipids for lipid-mediated transfer of the gene are DOTMA, DOPE and DC-Chol, for example). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein

25   associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g., capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, and proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem., 262: 4429-4432

30   (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA, 87: 3410-3414 (1990). For a review of known gene marking and gene therapy protocols, see Anderson *et al.*, Science, 256: 808-813 (1992). See also WO 93/25673 and the references cited therein.

Alternatively purified altered IGFBP can be administered to the mammal in a suitable carrier. the altered IGFBP may be administered orally parenterally, topically transdermally. It might be preferred to provide the altered IGFBP in slow release from.

5   Determination of appropriate dosages and formulation may be achieve by one of ordinary skill in the art using only routine experimentation. See for example Remington's Pharmaceutical Sciences (Martin E.E. ed, latest edition), Mack Publishing Co, Easton PA.

10   Further, included within the scope of the present invention is the co-administration of an altered IGFBP-2 together with a cytotoxic or anticancer agent. Such agents suitably include antimetabolites (e.g., 5-fluoro-uracil, methotrexate, fludarabine), antimicrotubule agents (e.g., vincristine, vinblastine, taxanes such as paclitaxel, docetaxel), an alkylating agent (e.g., cyclophasphamide, melphalan, biochoroethylnitrosurea, hydroxyurea),

15   platinum agents (e.g. cisplatin, carboplatin, oxaliplatin, JM-216, CI-973), anthracyclines (e.g., doxrubicin, daunorubicin), antibiolitics (e.g., mitomycin, idarubicin, adriamycin, daunomycin), topoisomerase inhibitiors (e.g., etoposide, camptothecins) or any other antineoplastic agents. (estramustine phosphate, prednimustine).

20   It is anticipated that altered IGFBP-2 used in combination with various anticancer drugs can give rise to a significantly enhanced cytotoxic effect on cancerous cells, thus providing an increased therapeutic effect. Specifically, as a significantly increased growth-inhibitory effect is obtained with the above disclosed combinations utilizing lower concentrations of the anticancer drugs compared to the treatment regimes in which

25   the drugs are used alone, there is the potential to provide therapy wherein adverse side effects associated with the anticancer drugs are considerably reduced than normally observed with the anticancer drugs used alone in larger doses.

Compounds of the present invention can be administered in a variety of ways including

30   enteral, parenteral and topical routes of administration. For example, suitable modes of administration include oral, subcutaneous, transdermal, transmucosal, iontophoretic,

intravenous, intramuscular, intraperitoneal, intranasal, subdural, rectal, vaginal, and the like.

Suitable pharmaceutically acceptable excipients include processing agents and drug

5   delivery modifiers and enhancers, such as, for example, calcium phosphate, magnesium

stearate, talc, monosaccharides, disaccharides, starch, gelatin, cellulose, methyl cellulose,

sodium carboxymethyl cellulose, dextrose, hydroxypropyl-β -cyclodextrin,

polyvinylpyrrolidinone, low melting waxes, ion exchange resins, and the like, as well as

combinations of any two or move thereof. Other suitable pharmaceutically acceptable

10   excipients are described in Remington's Pharmaceutical Sciences, Mack Pub. Co., N.J.

(1991), which is incorporated herein by reference.

In a sixth aspect the invention might be said to reside in a method of reducing IGF

mediated proliferation of a population of cancerous cell in the presence of IGF, by

15   contacting the population of cells with an altered IGFBP according to this invention.

Conditions that might be amenable to treatment in this way include cancers that are IGF

dependant and these may include certain cancers of the breast, prostate, colorectal, lung,

thyroid, ovaries, and brain as well as in childhood leukaemias, glioblastomas, and

20   neuroblastomas.

It is contemplated that treatment of say prostate cancer according to the present invention

may not necessarily be used on its own but as an adjunct to other methods.

25   By way of a shorthand notation the following three and one letter abbreviations for amino

acid residues are used in the specification as defined in Table 1.

Where a specific amino acid residue is referred to by its position in the polypeptide of an

·protein, the amino acid abbreviation is used with the residue number given in superscript

30   (i.e. Xaan)

TABLE 1

	Amino Acid	Three-letter Abbreviation	One letter Abbreviation
5			
	Alanine	Ala	A
	Arginine	Arg	R
	Asparagine	Asn	N
10	Aspartic Acid	Asp	D
	Cysteine	Cys	C
	Glutamine	Gln	Q
	Glutamic acid	Glu	E
	Glycine	Gly	G
15	Histidine	His	H
	Isoleucine	Ile	I
	Leucine	Leu	L
	Lysine	Lys	K
	Methionine	Met	M
20	Phenylalanine	Phe	F
	Proline	Pro	P
	Serine	Ser	S
	Threonine	Thr	T
	Tryptophan	Trp	W
25	Tyrosine	Tyr	Y
	Valine	Val	V

BRIEF DESCRIPTION OF THE DRAWINGS

30

Figure 1.   Schematic diagram of the hIGFBP-2 expression vector constructed from the mammalian expression vector pXMT2 (Rathjen *et al.,*

(1990); Whyatt *et al.,* (1993)). A colicin E1 origin of replication (ori) and the β-lactamase ampicillin resistance gene (Amp) enable selection and propagation in E. *coli.* Mammalian expression of the IGFBP-2 cDNA is driven by the adenovirus major late promoter

5 (MLP). The dihydrofolate reductase (DHFR) gene is present for selection. A 6 Histidine tag is encoded at the 3' end of the IGFBP-2 cDNA sequence.

Figure 2. Purified hIGFBP-2 and mutants were separated on a 12% tricine
10 SDS polyacrylamide gel. Proteins were stained with Coomassie blue (except for Des(114-170)His hIGFBP-2 which was stained with sypro ruby). All mutants migrated with the expected size as estimated by comparison with molecular size standards (Novex Broad range). A minor breakdown product was detected in this
15 particular K234AHis preparation.

Figure 3. Schematic of hIGFBP-2 and truncated hIGFBP-2 showing the conserved N- and C-cysteine domains connected by the linker domain. The know disulphide bonds (shown as transverse white
20 stripes) and residue numbers are indicated above. Potential cleavage and ECM sites are also identified.

Figure 4. BIAcore analysis of hIGFBP-2 and mutants binding to IGF-I. Human IGFBP-2 (at concentrations of 3.1, 6.25, 12.5, 25 and 50nM)
25 was allowed to associate with the Biosensor surface (70 resonance units of hIGFBP-2) for 300s (from t=150s) and then dissociated for 900s. Real time binding is measured in response units. Kinetic studies were performed at a flow rate of 30 μl/min to minimize mass transfer effects. The IGF-I-coated biosensor surface was regenerated
30 with 10mM HCl between binding cycles. For each binding curve the response obtained using control surfaces (no protein coupled) was subtracted.

Figure 5A   Analysis of susceptibility of truncated hIGFBP-2 to proteolysis in
             culture media conditioned by cancer cells. Truncated hIGFBP-2 and
             hIGFBP-2 were exposed to culture media of a) T84 colon cancer and
5   b) PC3 prostate cancer for 0, 3 or 24 hours at 37 degrees. Samples
             were separated by SDS polyacrylamide gel electrophoresis on 10%
             tricine gels and transferred to nitrocellulose. hIGFBP-2 and cleavage
             products were detected with an anti-IGFBP-2 polyclonal antibody
             (left). hIGFBP-2 migrates at 34kDa whereas Des(114-170)His
10   migrates at 20kDa. A dimer is present in hIGFBP-2 preparations.
             Proteolytic fragments range in size between 14 to 20 kDa. Densities
             of bands indicated on the blots were quantitated using the NIH
             image program and amounts of uncleaved or cleaved hIGFBP-2
             graphed (right).

15

Figure 5B   Analysis of susceptibility of truncated hIGFBP-2 to proteolysis in
             culture media conditioned by cancer cells. Truncated hIGFBP-2 and
             hIGFBP-2 were exposed to culture media of c) DU145 and d)
             LNCaP prostate cancer cell lines for 0, 3 or 24 hours at 37 degrees.
20   Samples were separated by SDS polyacrylamide gel electrophoresis
             on 10% tricine gels and transferred to nitrocellulose. hIGFBP-2 and
             cleavage products were detected with an anti-IGFBP-2 polyclonal
             antibody (left). hIGFBP-2 migrates at 34kDa whereas Des(114-
             170)His migrates at 20kDa. A dimer is present in hIGFBP-2
25   preparations. Proteolytic fragments range in size between 14 to 20
             kDa. Densities of bands indicated on the blots were quantitated using
             the NIH image program and amounts of uncleaved or cleaved
             hIGFBP-2 graphed (right), and

30   Figure 6   Proliferation of HT-29 colorectal cells measured by Cell Titre Glo
                  Assay (Promega). Apoptosis was induced with 5mM butyrate and
                  the ability of IGF-1 to promote cell survival was measured. Native

IGFBP-2, DES(114-170) and DES (114-170) K180A K181A were added to cells treated with IGF-1 at various concentrations (0, 0.1, 0.3 and 0.65nM) in the presence of butyrate. Results are expressed as a percentage of proliferation in the presence of culture medium

5   alone. As Des (114-170) and Des (114-170) K180A K181A have two fold lower affinity for IGF-I and IGF-II respectively the percentage proliferation for these treatments was adjusted accordingly.

10   DETAILED DESCRIPTION OF THE INVENTION

<u>Materials and Methods</u>

Mutagenesis and subcloning

Mutations of cDNA encoding hIGFBP-2 in the pBluescript vector (Stratagene, La Jolla,

15   CA, USA) were introduced using the Quikchange mutagenesis method (Stratagene). The following oligonucleotides were used to introduce the lysine (K) to alanine (A) mutations and the deletion mutant Des(114-170)His:

K180A K181AHis   Forward 5'CTT GGC CTG GAG GAG CCT GCC GCC CTG CGA CCA CCC CCT

20   3'

[SEQ ID No 19]

              Reverse 5'AGG GGG TGG TCG CAG GGC GGC AGG CTC CTC CAG GCC AAG

3'

[SEQ ID No 20]

25

K227AHis   Forward 5'ATC CCC AAC TGT GAC GCC CAT GGC CTG TAC ACC 3'

[SEQ ID No 21]

              Reverse 5'GGT GTA CAG GCC ATG GGC GTC ACA GTT GGG GAT 3'

[SEQ ID No 22]

K234AHis
[SEQ ID No 23]

Forward 5'GGC CTG TAC AAC CTC GCC CAG TGC AAG ATG TCT 3'

Reverse 5'AGA CAT CTT GCA CTG GGC GAG GTT GTA CAG GCC 3'

5   [SEQ ID No 24]

K237AHis
[SEQ ID No 25]

Forward 5'AAC CTC AAA CAG GCC ATG TCT CTG AAC GGG 3'

Reverse 5'CCC GTT CAG AGA CAT GGC GCA CTG TTT GAG GTT 3'

10 [SEQ ID No 26]

Des(114-170)His
[SEQ ID No 27]

Forward1 5'GTT GCA GAC AAT GGC GCC GGC CAC TCA GAA GAA GCC 3'

Reverse1 5'GCC TCC TTC TGA GTG GCC GGC GCC ATT GTC TGC AAC 3'

[SEQ ID No 28]

15   Forward2 5'CGG CAC ATG GGC AAG GCC GGC AAG CAT CAC CTT 3'

[SEQ ID No 29]

Reverse2 5'AAG GTG ATG CTT GCC GGC CTT GCC CAT GTG CCG 3'

[SEQ ID No 30]

20 The deletion mutant Des(114-170)His was generated by sequentially introducing two
    NaeI restriction sites in the cDNA encoding residues 114 and 170 respectively. The new
    clone was then digested with NaeI and religated to delete out the sequence between these
    sites.

25 The cDNA clones encoding resultant mutant IGFBPs were transformed into DH5α E.
    coli. Clones were sequenced to confirm correct introduction of mutations. They were
    subsequently subcloned into the pXMT-2 vector using XhoI and EcoRI restriction sites
    and transformed into DH5α E. *coli* (see Figure 1; Rathjen P.D. *et al.,* (1990); Whyatt
    L.M. *et al.,* (1993)). Mutant IGFBP-2 proteins were expressed upon transient
30 transfection of COS-1 monkey kidney cells (ATCC:CRL 1650) with the mutant IGFBP-2
    cDNAs. Cos-1 cells are cultured in DMEM (GIBCO) + 10% FCS. The method of culture
    and purification is described in Forbes *et al.,* (1998)

Purification and Analysis of purity

Proteins were purified using standard Nickel affinity purification techniques taking advantage of a 6 histidine tag at the C-terminus of each protein. Purification is from

5 culture medium as the IGFBP is secreted (Forbes et al, 1998). Following elusion from the nickel column, proteins were further purified using reverse phase high performance liquid chromatography (HPLC). Purity was analysed by rpHPLC, SDS PAGE and mass spectrometry. The mass of each mutant was determined by electrospray mass spectrometry (by Dr. Chris Bagley, Hanson Centre) and found to be correct (generally

10 within the limits of the mass spec=1 mass unit/10,000 daltons).

Measurement of IGF binding affinities

IGF binding affinities of hIGFBP-2 and mutants were determined by surface plasmon resonance using the BIAcore with IGF-I or IGF-II coupled to the sensor surface (for

15 details of method see Carrick *et al.*, (2001). IGF-I or IGF-II (70RU) was coupled to a CM-5 biosensor chip (BIAcore Inc) via amine groups using standard coupling procedures (Lofas and Johnsson, 1990). Briefly, at 5μl/min a CM5 chip was activated with 35μl NHS (0.4mg)/EDC (2.6mg) and then 35μl IGF (10μg/ml) was coupled in 10mM sodium acetate pH 4.5. Unreacted groups were inactivated with 35μl 1M ethanolamine-HCl, pH

20 8.5. Kinetic studies with a range of hIGFBP-2 or mutant concentrations (50, 25, 12.5, 6.25 and 3.1nM) were performed at 40μl/min to minimize mass transport effects with 300 secs allowed for association and 900 secs for dissociation. The IGF surface was regenerated with 10mM HCl.

25 *Proteolysis Assay*

The source of proteases for the proteolysis assays was conditioned medium of cancer cells. Cells were grown to confluence in the presence of foetal calf serum. (T84 cells are grown in DMEM: Ham's F12 (50:50 v:v) with 10% foetal bovine serum FBS; LNCaP were grown in RPMI+6%FBS; PC3 and DU145 were grown in DMEM+10%FBS, all

30 media and FBS are from GIBCO). Cells were then washed 2x2 hours in serum free culture medium. Cells were then cultured for 3 days in serum free conditions and the medium was collected. Conditioned medium was concentrated approximately 10 fold

using a centricon-10 (Millipore Corp, MA USA). Purified hIGFBP-2 or mutants thereof (250ng in 2μl) were mixed with conditioned medium for 24 hours at 37°C to allow proteolysis. Proteins were separated on 12% tricine SDS polyacrylamide gels and transferred to nitrocellulose. Nitrocellulose filters were probed with a specific polyclonal

5   anti-IGFBP-2 antibody (raised in our laboratory) to detect IGFBP-2 and IGFBP-2 fragments. A secondary goat anti-rabbit antibody conjugated to avidin alkaline phosphatase (Sigma) was used to detect the anti-IGFBP-2 antibody. Substrates for avidin alkaline phosphatase (nitroblue tetrazolium and 5 bromo 4 chloro 3-indolyl phosphate p-toluidine salt) were added and coloured bands indicated presence of IGFBP-2.

10

Matrix binding assay

Heparin was biotinylated using biocytin hydrazine (Pierce) using conditions recommended by the manufacturer. Following the reaction the biotinylated heparin was concentrated using a centricon-3 (Millipore Corp, MA USA) and was dialysed against

15   H_2O. Biotinylated heparin was coupled to a streptavidin biosensor chip in 0.3M NaCl and HBS (hepes buffered saline containing surfactant, BIAcore Inc.). hIGFBP-2 and mutants at different concentrations (6.25nM to 300nM) were injected at 10μl/min. Regeneration of the surface was achieved with 2M NaCl.

20   *Proliferation of HT-29 colorectal cells*

Cells are plated at 12,000 cells per well in 96 well plates in RPMI (GIBCO)+10%FCS (foetal calf serum), grown for 2 days, washed in serum free RPMI for 3 hours and then treated with butyrate (5mM, Sigma) or butyrate with IGF-I at various concentrations in RPMI+5% BSA. In this experiment different amounts of IGFBP-2 or mutant IGFBP-2

25   were added to the butyrate+IGF-1 treated cells. Proliferation is measured using the Cell titre Glo kit from Promega. This measures ATP levels basically. IGF rescues cells from apoptosis and the binding proteins (native or mutant) inhibit the ability of IGF to rescue cells from apoptosis (sequester IGF away from the receptor).

Results and Discussion

Cloning, expression, purity and IGF binding affinities

Five mutants have been designed for introduction of protease resistance or interruption of matrix binding (K180A K181AHis, K227AHis, K234AHis, K237AHis, Des(114-

5   170)His). These were purified to homogeneity (Figure 2) and subjected to mass spectral analysis to confirm they had the expected mass. The residues K180 and K181 are potential sites of protease cleavage (Ho, J.P. & Baxter, R.C. (1997) and are also possibly involved in matrix binding (Hodgkinson, et al (1994)). K227, K234 and K237 are residues in the analogous regions of IGFBP-3 and –5 corresponding to matrix binding

10   motifs. The potential sites of proteolytic cleavage and matrix binding are highlighted in Figure 3.

The purified mutants were tested for their ability to bind IGF-I by BIAcore analysis (Figure 4). All mutants have similar affinities to native hIGFBP-2. Mutant K237AHis has about 2 fold higher affinity for both IGF-I and IGF-II and Des(114-170)His has a 5

15   fold or 2 fold decrease in affinity for IGF-I and IGF-II respectively (Tables 2 and 3).

Table 2 shows the kinetic constants obtained from BIAcore analysis of hIGFBP-2 and mutant hIGFBP-2 binding to IGF-I. Data was analysed using BIAevaluation software 3.0

20   and fit to a Langmuir 1:1 binding model. The dissociation constant (K_D) was determined from the calculation of k_d/k_a, where k_a is the association rate and k_d is the dissociation rate. Relative K_D is equal to K_D of hIGFBP-2/K_D of hIGFBP-2 mutant.

Table 2.

	k_a $\times 10^5$ (1/Ms)	k_d $\times 10^{-4}$ (1/s)	k_D $\times 10^{-10}$ (M)	Rel.K_D
hIGFBP-2	1.8	1.74	9.67	1.0
K180A K181A	6.41	6.8	11.1	0.87
K227A	1.91	1.37	7.17	1.34
K234A	1.69	2.52	14.9	0.64
K237A	7.24	3.06	4.22	2.29

Des(114-170)	1.17	4.25	36.3	0.26

Table 3. Kinetic constants obtained from BIAcore analysis of hIGFBP-2 and mutant
hIGFBP-2 binding to IGF-II. Data was analysed using BIAevaluation software 3.0 and fit
to a Langmuir 1:1 binding model. The dissociation constant (K_D) was determined from
the calculation of k_d/k_a, where k_a is the association rate and k_d is the dissociation rate.
Relative K_D is equal to K_D of hIGFBP-2/K_D of hIGFBP-2 mutant.

Table 3

	k_a $\times 10^5$ (1/Ms)	k_d $\times 10^{-4}$ (1/s)	k_D $\times 10^{-10}$ (M)	Rel.K_D
hIGFBP-2	2.38	1.4	5.89	1.0
K180A K181A	6.51	5.58	8.57	0.68
K227A	2.09	0.96	4.61	1.27
K234A	1.81	2.86	15.8	0.37
K237A	7.24	1.23	2.01	2.9
Des(114-170)	1.14	1.3	11.4	0.51

Protease Assays

The mutant binding proteins were tested for protease sensitivity in the assay described in
materials and methods. We first analysed the truncation mutant Des(114-170)His and
observed protease resistance in a number of conditioned media including T84, HT29,
CaCO (all colon cancer cells) and PC3 (prostate cancer cell line). Table 4 outlines
which cell lines were used, the relative amount of protease activity (qualitative from
observations of gels) and which conditioned media contained proteases which are no
longer able to cleave the truncation mutant.

Table 4. List of cell lines used as sources of conditioned media containing proteolytic
activity. Cell lines are grouped in to cancer types. A qualitative score is given to each
cell line indicating the amount of proteolytic activity evident upon incubation with

hIGFBP-2 (central column). If the truncation of hIGFBP-2 (Des(114-170)His hIGFBP-2) resulted in protection against cleavage by conditioned media compared with hIGFBP-2 then this is indicated in the column on the right.

5 Table 4.

	Proteolytic Activity	Protection
Prostate Cancer		
LNCaP	***	No
PC3	*	Yes
DU145	***	No
Colon Cancer		
HT29	*	Yes
SW480	**	No
LIM1215	**	Not sure
CaCo	*	Yes
T84	***	Yes
Breast Cancer		
MCF7	*	No

Importantly, there was a significant amount of easily detectable protease activity in the T84 cell line conditioned medium (Figure 5A and 5B). The truncation mutant was

10 clearly resistant to proteolysis in this medium. Proteolysis of hIGFBP-2 was also easily detected in PC3 conditioned medium and the truncation mutant was also resistant to proteolysis by this medium (Figure 5A). In other cell lines there was less proteolytic activity making detection of protease resistance more difficult (eg LIM1215). In other cell lines the truncation mutant was clearly proteolysed (Figure 5B).

15

These results highlight the fact that each cell line produces a different array of proteases. It is not known which protease is cleaving hIGFBP-2 in the T84 and PC3 media. The

cleavage product in T84 medium corresponds to a C-terminal fragment of hIGFBP-2 as detected by an antibody specific for C-terminal residues. We have tested the other mutants in the T84 conditioned medium for protease resistance. As these residues lie outside the 114-170 truncation it was not surprising that none were resistant to

5   proteolysis, suggesting that cleavage does not occur at K180, K181, K227, K234, K237.

Heparin binding

We analyzed matrix binding using the commonly used model system of heparin binding. We analyzed heparin binding using the BIAcore. Preliminary data show that the K234A

10   mutation reduces heparin binding 5 fold (Fig 8) and the K180A, K181A mutation has a great effect on heparin binding. This data indicates that there are probably 2 heparin binding sites on IGFBP-2.

Table 5. Heparin binding affinities of hIGFBP-2 and K234AHis IGFBP-2 were measured

15   by surface plasmon resonance. Data was analysed using BIA evaluation software 3.0 and fit to a Langmuir 1:1 binding model. The dissociation constant (K_D) was determined by the calculation of k_d/k_a, where k_a is the association rate and k_d is the dissociation rate.

Table 5 Heparin binding by gIGFBP-2 and mutants

20

	K_D (M)
hIGFBP-2	1×10^{-8}
K234A hIGFBP-2	4.82×10^{-8}

Proliferation of HT-29 colorectal cells

The assay shows that HT-29 colorectal cancer cells undergo apoptosis in 5mM Butyrate.

25   Addition of IGF-I rescues cells from butyrate induced apoptosis in a dose dependent manner. Additional IGFBP-2 inhibits the ability of IGF-I to rescue cells from butyrate induced apoptosis by sequestering the IGF away from the IGF receptor. The mutants Des (114-170) and Des (114-170) K180A K181A are more effective at inhibiting the action of IGF-I. This assay shows little difference between Des (114-170) and Des (114-170)

K180A K181A suggesting the greatest benefit is the resistance to proteolysis conferred to the molecule by removal of protease cleavage sites. Mutation of positions K180A and K181A could also protect from further proteolysis or inhibit interaction with the extracellular matrix. However, under the conditions of this assay it is not possible to

5   detect a significant difference between Des (114-170) and Des (114-170) K180A K181A.

REFERENCES

Arai *et al.,. Endcrinology* **137**, 4571-4575 (1996)

Arai *et al., J. Biol. Chem.* **269**, 20388-20393 (1996)

10   Baserga, *Exp. Cell Res.* **253(1)**,1-6 (1999)

Braulke, *Horm. Metab. Res.* **31(2-3)**, 242-246 (1999)

Byun *et al., J Clin Endocrinol Metab* 85(1):373-81 (2000).

Chan *et al., Science* **279**, 563-566 (1998)

Cardin. & Weintraub *Arteriosclerosis* **9**, 21-32 (1989).

15   Carrick *et al., J. Biol. Chem.* **276**, 27120-27128 (2001)

Cohen *et al., J. Clin. Endocrinol. Metab.* **79**, 1410-1415(1994)

DiGiovanni *et al., PNAS* **97**, 3455-3460 (2000)

Elminger *et al., Mol. Cell. Endocrinol.* **175(1-2)**, 211-218 (1999)

Firth *et al., J. Biol. Chem.* **273**, 2631-2638 (1998)

20   Forbes *et al., J. Biol. Chem.* 273, 4647-4652 (1998)

Ho & Baxter, *Clin. Endocrinol.* 46, 333-342 (1997)

Ho & Baxter *Endocrinology* **138**, 3811-3818 (1997).

Hobba *et al., J. Biol. Chem.* **273**:19691-19698 (1998).

Hodgkinson *et al. J. Mol. Endocrinol.* **13**, 105-112 (1994);

25   Imai *et al., J. Clin. Invest.* 100(10), 2596-2605 (1997)

Kanety, *et al. J. Clin. Endocrinol. Metab.* **77**, 229-233 (1993).

Lofas and Johnsson, *J. Chem. Soc. Chem. Commun.* **21**, 1526-1528 (1990)

Menouny *et al., Endocrinology* **138**, 683-690 (1997).

Michell *et al., Br. J. Cancer* **76**, 60-66 (1997).

30   Nunn *et al., J. Cell. Physiol.* **171**, 196-204 (1997).

Rathjen *et al., Cell* **62(6)**,1105-1114 (1990)

Russo *et al. Endocrinology* **138**, 4858-4867 (1997)

Sepp-Lorenzino, *Breast Cancer Res. Treat.* **47(3)**, 235-253 (1998)

Thrasher *et al.*, *J. Urol.* **155**, 999-1003 (1996)

Wang *et al.*, *Nature* **372**, 464-467 (1994)

Whyatt *et al.*, *Mol. Cell. Biol.* **13**, 7971-7976 (1993)

5   Zeslawski *et al.*, *EMBO J.* **20**, 3638-44 (2001)